

# Ph. Eur. Monograph 0923: Azithromycin Related Substances on Gemini™ NX-C18 and Durashell C18(L) Columns

Krishna Chaitanya Routhu<sup>1</sup>, Swetha Kotikalapudi<sup>1</sup>, Heiko Behr, PhD<sup>2</sup>, and Bryan Tackett, PhD<sup>3</sup> <sup>1</sup>India Phenologix Lab, Phenomenex India, Hitech Defence and Aerospace Park Industrial Area, Mahadeva Kodigehalli, Holbi, Jala Taluka, Bengaluru 562149, India

<sup>2</sup>Phenomenex Ltd. Deutschland, Zeppelinstr. 5, 63741 Aschaffenburg, Germany

<sup>3</sup>Phenomenex Inc., 411 Madrid Ave., Torrance, CA 90501 USA



Azithromycin is a broad-spectrum macrolide antibiotic which is commonly used for the treatment of bacterial infections. In this application note we show the separation of Azithromycin from its related substances following Ph. Eur. Monograph 1649. A Gemini 5 μm NX-C18 column and a Durashell 5µm C18(L) column were used and compared to the Waters® XTerra® MS C18, originally used in the monograph. To decrease the run time and improve efficiency upon the Ph. Eur. Method for the analysis of Azithromycin, an optimized method that fell within the Ph. Eur. Allowable adjustments for this gradient method was designed. Gemini 5 um NX-C18 and Durashell 5 μm C18(L) columns were used to demonstrate the standard Azithromycin Ph. Eur. Method, while Gemini 3 µm NX-C18 column was used for the adjusted method conditions.

The use of a 150 x 4.6 mm, 3 µm of the Gemini NX-C18 column is a new (European Pharmacopoeia 11.0) allowable adjustment in a gradient method to a 250 x 4.6 mm, 5  $\mu m$  since the L/dp ratio (150 mm / 3  $\mu$ m = 50,000) is within the allowable range of -25 to +50 % of L/dp ratio (250 mm / 5  $\mu$ m = 50,000) for the original 5  $\mu$ m column used to elucidate the related substances method. The gradient and flow rate were calculated as recommended by Ph. Eur. Chapter 2.2.46 (revised July 2022) for the 150 x 4.6 mm, 3 μm column.

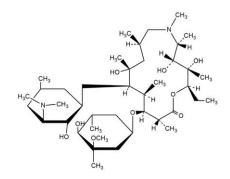
The columns used under the published monograph conditions met and surpassed the system suitability requirement for separation between Impurity F and Impurity J of a minimum for H<sub>a</sub>/H<sub>a</sub> of 1.4, where H<sub>-</sub> = height above the baseline of the peak for impurity J. and H<sub>-</sub> = height above the baseline of the lowest point of the curve separating this peak from the peak due to impurity F. Relative to the XTerra MS 5 um C18 column, the Durashell 5 um C18(L) and Gemini 5 um NX-C18 column gave similar separation.

The results show that both the Gemini 5 μm NX-C18 and Durashell 5 μm C18(L) columns are suitable under the conditions outlined in the Ph. Eur. monograph for Azithromycin. A baseline resolution was achieved between Impurity F and Impurity J in Reference Solution (b) for the Gemini 5 μm NX-C18, Durashell 5 μm C18(L), and XTerra MS 5 μm C18 columns. Therefore, a Hp/Hv value could not be calculated, and resolution between the two peaks is reported instead. The H<sub>p</sub>/H<sub>v</sub> ratio is used because baseline resolution is not typically achieved between Impurity F and Impurity J, and a resolution value can therefore not be reported. With the Gemini 3 µm NX-C18, 150 x 4.6 mm column we demonstrated a reduction in total analysis time by 64 % (from 93 min to 34 min), by implementing the changes to the gradient and flow rate as recommended by the allowable adjustments recommended in Ph. Eur. Chapter 2.2.46.

All the reference solutions were prepared as indicated in Ph. Eur. monograph 1649 for Azithromycin. The following certified reference standards (CRS) were purchased from the European Directorate for the Quality of Medicines & HealthCare (EDQM) - Council of Europe; Postal address: 7 Allee Kastner CS 30026 F - 67081 Strasbourg (France):

- Y0000637, Azithromycin for Peak Identification CRS
- Y0000642, Azithromycin for System Suitability CRS
- Y0000306, Azithromycin CRS

Figure 1. Azithromycin Structure





## **LC-UV Conditions – Original Method**

Columns: Gemini 5 µm NX-C18 (00G-4454-E0) Durashell 5 μm C18(L) (DC952505-L)

Waters XTerra 5 µm MS C18

Dimensions: 250 x 4.6 mm

Mobile Phase: Mobile Phase (Table 1) Gradient: Time (min) 55 25 30 60 75 80 93

Flow Rate: 1.0 mL/min Injection: 50 uL Temperature: 60 °C Detector: UV @ 210 nm System: Waters Arc® HPLC

## **LC-UV Conditions - Adjusted Method**

Columns: Gemini 3 µm NX-C18 (00F-4453-E0)

Dimensions: 150 x 4.6 mm

Mobile Phase: Mobile Phase (Table 1) Gradient: Time (min) 50 55 10.8 60 29.16 50 33.48

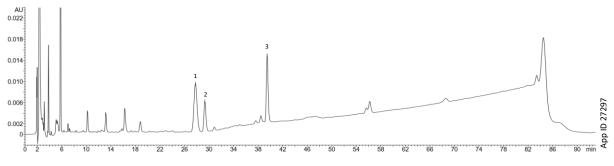
Flow Rate: 1.667 mL/min Injection: 30 µL Temperature: 60 °C Detector: UV @ 210 nm System: Waters Arc HPLC

Table 1. Preparation of Test and Reference Solutions

Solution	Composition
Mobile Phase	A: 1.80 g/L solution of Anhydrous Disodium Hydrogen Phosphate R adjusted to pH 8.9 with dilute Phosphoric Acid R or with dilute Sodium Hydroxide solution R.
	B: Methanol R1 / Acetonitrile R1 (25:75, v/v).
Diluent Buffer	Prepare a 1.73 g/L solution of Ammonium Dihydrogen Phosphate R adjusted to pH 10.0 with Ammonia R.
Diluent	Diluent Buffer / Acetonitrile R1 / Methanol R1 (35:30:35, v/v/v).
Test Solution	Dissolve 0.200 g of Azithromycin CRS in <b>Diluent</b> and dilute to 25.0 mL with <b>Diluent</b> .
Reference Solution (a)	Dilute 1.0 mL of Test Solution to 100.0 mL with Diluent.
Reference Solution (b)	Dissolve the contents of a vial of Azithromycin for System Suitability CRS (containing impurities F, H and J) in 1.0 mL of the <b>Diluent</b> and sonicate for 5 min.
Reference Solution (c)	Dissolve 8.0 mg of Azithromycin for Peak Identification CRS (containing impurities A, B, C, E, F, G, I, J, L, M, N, O and P) in 1.0 mL of <b>Diluent</b> .

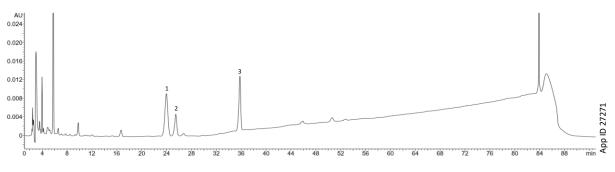
Figure 1. Related Substances Analysis Reference Solution (b)

# Gemini™ 5 μm NX-C18 Column



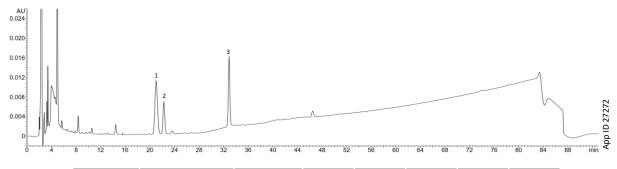
Peak No.326896	Analyte	Retention Time (min)	Area	Height	Symmetry Factor	H <sub>P</sub> /H <sub>v</sub>	Resolution
1	Impurity F	27.78	326896	9103	1.08	Undefined	2.0
2	ImpurityJ	29.32	129182	5650	1.11	Ondermed	
3	Impurity H	39.48	250292	12596	1.15	=	=
N = 3 Injections							

# Durashell 5 μm C18(L) Column



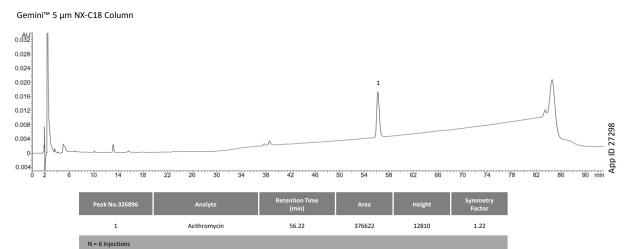
Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor	H <sub>P</sub> /H <sub>v</sub>	Resolution
1	Impurity F	23.97	301317	8701	0.94	Undefined	2.0
2	Impurity J	25.48	112599	4210	0.88	Ondermed	2.0
3	Impurity H	35.80	238913	10204	0.84	=	Ē
N = 3 Injections							

# XTerra® 5 μm MS C18 Column



Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor	H <sub>p</sub> /H <sub>v</sub>	Resolution
1	Impurity F	20.71	321082	10738	1.07	Undefined	2.0
2	Impurity J	22.03	129352	6353	1.11	Ondermed	2.0
3	Impurity H	32.88	241592	13971	1.00	=	=
N = 3 Injections							

Figure 3. Related Substances Analysis Reference Solution (a)



# Durashell 5 μm C18(L) Column AU 0.032 0.028 0.024 0.020 0.016 0.012 0.008 App ID 27273 0.004 0.004 Azithromycin 48.82 327614 12234 0.95 N = 6 Injections

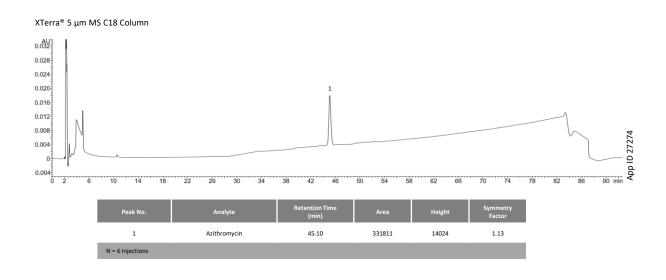
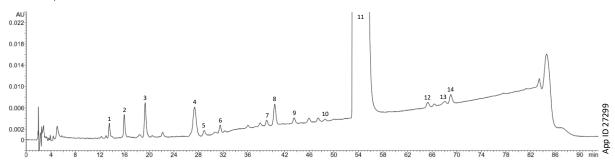


Figure 4. Related Substances Analysis Reference Solution (c)

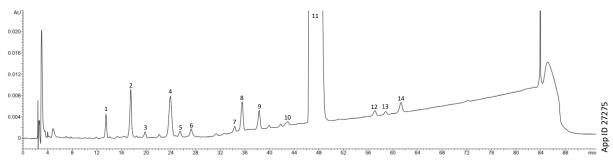
# Gemini™ 5 μm NX-C18 Column



Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor
1	Impurity L	13.49	35997	2654	1.06
2	Impurity M	15.92	66126	4204	1.33
3	Impurity E	19.32	133538	6454	1.42
4	Impurity F	27.36	207053	5407	0.94
5	Impurity J	28.92	26093	994	1.16
6	Impurity I	31.51	28189	1454	1.09
7	Impurity C	39.08	22691	1036	1.12

Peak No. Analyte		Retention Time (min)	Area	Height	Symmetry Factor
8	Impurity N	40.39	98387	3862	1.06
9	Impurity A	43.54	25649	1054	1.14
10	Impurity P	48.55	9785	387	1.11
11	Azithromycin	53.24	31502309	347221	5.09
12	Impurity O	65.27	27489	960	1.04
13	Impurity G	68.05	18545	500	0.78
14	Impurity B	69.02	47897	1657	1.17

# Durashell 5 μm C18(L) Column

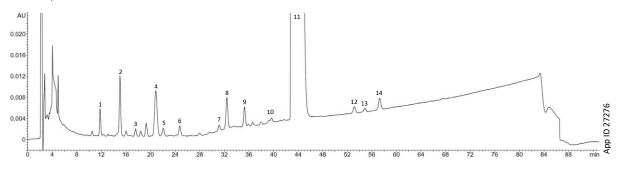


Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor
1	Impurity L	13.47	65006	4501	0.95
2	Impurity M	17.49	177207	9006	0.91
3	Impurity E	19.82	24983	1142	0.88
4	Impurity F	23.91	242104	7547	0.92
5	Impurity J	25.49	23922	1020	1.05
6	Impurity I	27.30	39111	1448	1.20
7	Impurity C	34.35	20898	993	0.78

Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor
8	Impurity N	35.56	125103	5337	0.87
9	Impurity A	38.31	80042	3434	0.90
10	Impurity P	42.96	8056	430	0.98
11	Azithromycin	46.50	31348153	445184	6.17
12	Impurity O	57.09	29732	976	0.86
13	Impurity G	58.84	16137	576	0.81
14	Impurity B	61.31	64709	1890	0.82

Figure 4 Cont'd. Related Substances Analysis Reference Solution (c)

# XTerra® 5 μm MS C18 Column

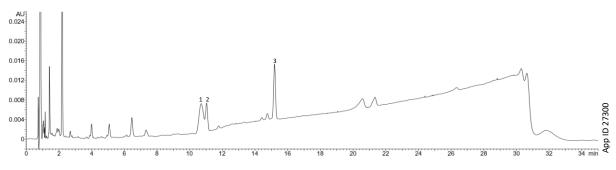


Peak No.	Analyte Retention Time (min)		Area	Height	Symmetry Factor
1	Impurity L	11.78	67136	5086	1.13
2	Impurity M 15.00 165277		11008	1.08	
3	Impurity E	17.538	23815	1414	1.06
4	Impurity F	20.813	248780	8497	1.08
5	Impurity J	22.040	31183	1462	0.91
6	Impurity I	24.719	37962	1778	1.18
7	Impurity C	31.101	23412	1091	1.02

Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor
8	Impurity N	32.38	124632	5759	0.96
9	Impurity A	35.24	33246	3533	1.00
10	Impurity P	39.66	9956	576	1.09
11	Azithromycin	42.86	31681423	446080	7.45
12	Impurity O	53.08	30859	1191	0.99
13	Impurity G	54.78	15919	691	0.93
14	Impurity B	57.21	65161	2126	1.03

Figure 5. Related Substances Analysis Reference Solution (b) – Adjusted Method

Gemini™ 3 μm NX-C18 Column



Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor	H <sub>p</sub> /H <sub>v</sub>	
1	Impurity F	10.70	109558	5921	-	2.26	
2	ImpurityJ	11.04	55195	5808	-		
3	Impurity H	15.20	87685	11129	1.0	÷	
N = 3 Injections							

Figure 6. Related Substances Analysis Reference Solution (a) – Adjusted Method

Gemini™ 3 μm NX-C18 Column

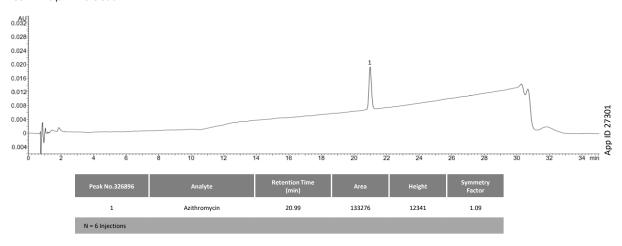
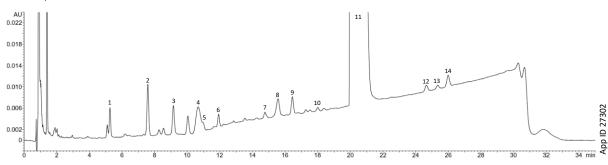


Figure 7. Related Substances Analysis Reference Solution (c) – Adjusted Method

Gemini 3  $\mu m$  NX-C18 Column



F	Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor	Peak No.	Analyte	Retention Time (min)	Area	Height	Symmetry Factor
	1	Impurity L	5.26	26525	5058	1.07	8	Impurity N	15.56	43214	3218	0.79
	2	Impurity M	7.58	71923	9615	1.03	9	Impurity A	16.44	29139	3220	0.97
	3	Impurity E	9.15	44766	5366	1.00	10	Impurity P	18.00	6623	703	0.84
	4	Impurity F	10.67	96085	4785	-	11	Azithromycin	20.03	13100153	377903	6.43
	5	Impurity J	10.95	12438	1700	-	12	Impurity O	24.65	14235	1184	0.78
	6	Impurity I	11.92	16517	2293	1.01	13	Impurity G	25.35	8286	720	0.78
	7	Impurity C	14.76	11133	1117	1.12	14	Impurity B	25.99	24223	2096	0.90

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t: +420 272 017 077 cz-info@phenomenex.com

### Denmark

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### Finland

t: +358 (0)9 4789 0063 nordicinfo@phenomenex.com

France t: +33 (0)1 30 09 21 10 franceinfo@phenomenex.com

t: +49 (0)6021-58830-0 anfrage@phenomenex.com

## **Hong Kong**

t: +852 6012 8162 hkinfo@phenomenex.com

### India

t: +91 (0)40-3012 2400 indiainfo@phenomenex.com

### Indonesia

t: +62 21 5019 9707 indoinfo@phenomenex.com

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Italy t: +39 051 6327511 italiainfo@phenomenex.com

### Japan

t: +81 (0) 120-149-262 jpinfo@phenomenex.com

Luxembourg t: +31 (0)30-2418700 nlinfo@phenomenex.com

### Mexico

t: 01-800-844-5226 tecnicomx@phenomenex.com

# The Netherlands

t: +31 (0)30-2418700 nlinfo@phenomenex.com

# **New Zealand**

t: +64 (0)9-4780951 nzinfo@phenomenex.com

**Norway** t: +47 810 02 005 nordicinfo@phenomenex.com

## Poland

t: +48 22 104 21 72 pl-info@phenomenex.com

Portugal t: +351 221 450 488 ptinfo@phenomenex.com

Singapore t: +65 6559 4364 sginfo@phenomenex.com

**Slovakia** t: +420 272 017 077 sk-info@phenomenex.com

### Spain

t: +34 91-413-8613 espinfo@phenomenex.com

### Sweden

t: +46 (0)8 611 6950 nordicinfo@phenomenex.com

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t: +41 (0)61 692 20 20 swissinfo@phenomenex.com

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t: +886 (0) 0801-49-1246 twinfo@phenomenex.com

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t: +66 (0) 2 566 0287 thaiinfo@phenomenex.com

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